

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 10/508,965  
Source: IFWO  
Date Processed by STIC: 11/28/06

# ***ENTERED***



IFWO

## RAW SEQUENCE LISTING

DATE: 11/28/2006

PATENT APPLICATION: US/10/508,965

TIME: 13:00:13

Input Set : A:\051530-5007-US Sequence Listing.txt

Output Set: N:\CRF4\11282006\J508965.raw

3 <110> APPLICANT: Transmolecular, Inc.  
 4 GONDA, Matthew A  
 5 GREENWOOD, John D  
 7 <120> TITLE OF INVENTION: Recombinant Expression Vectors for Functional Nav1.9 Sodium Channels  
 9 <130> FILE REFERENCE: 51530-5007-US  
 11 <140> CURRENT APPLICATION NUMBER: US 10/508,965  
 C--> 12 <141> CURRENT FILING DATE: 2004-09-23  
 14 <150> PRIOR APPLICATION NUMBER: PCT/US03/08611  
 15 <151> PRIOR FILING DATE: 2003-03-20  
 17 <150> PRIOR APPLICATION NUMBER: US 60/365,550  
 18 <151> PRIOR FILING DATE: 2002-03-20  
 20 <160> NUMBER OF SEQ ID NOS: 35  
 22 <170> SOFTWARE: PatentIn version 3.1  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 5905  
 26 <212> TYPE: DNA  
 27 <213> ORGANISM: Rattus norvegicus  
 29 <220> FEATURE:  
 30 <221> NAME/KEY: CDS  
 31 <222> LOCATION: (52)..(5349)  
 34 <400> SEQUENCE: 1  
 35 tctggagcca tacggtgccc tgatcctctg taccaggaag acaggggtgaa g atg gag 57  
 36 Met Glu  
 37 1  
 39 gag agg tac tac ccg gtg atc ttc ccg gac gag cgg aat ttc cgc ccc 105  
 40 Glu Arg Tyr Tyr Pro Val Ile Phe Pro Asp Glu Arg Asn Phe Arg Pro  
 41 5 10 15  
 43 ttc act tcc gac tct ctg gct gcc ata gag aag cgg att gct atc caa 153  
 44 Phe Thr Ser Asp Ser Leu Ala Ala Ile Glu Lys Arg Ile Ala Ile Gln  
 45 20 25 30  
 47 aag gag agg aag aag tcc aaa gac aag gcg gca gct gag ccc cag cct 201  
 48 Lys Glu Arg Lys Lys Ser Lys Asp Lys Ala Ala Ala Glu Pro Gln Pro  
 49 35 40 45 50  
 51 cgg cct cag ctt gac cta aag gcc tcc agg aag tta cct aag ctt tat 249  
 52 Arg Pro Gln Leu Asp Leu Lys Ala Ser Arg Lys Leu Pro Lys Leu Tyr  
 53 55 60 65  
 55 ggt gac att ccc cct gag ctt gta gcg aag cct ctg gaa gac ctg gac 297  
 56 Gly Asp Ile Pro Pro Glu Leu Val Ala Lys Pro Leu Glu Asp Leu Asp  
 57 70 75 80  
 59 cca ttc tac aaa gac cat aag aca ttc atg gtg ttg aac aag aag aga 345  
 60 Pro Phe Tyr Lys Asp His Lys Thr Phe Met Val Leu Asn Lys Lys Arg  
 61 85 90 95  
 63 aca att tat cgc ttc agc gcc aag cgg gcc ttg ttc att ctg ggg cct 393

*see p. 6*

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64	Thr	Ile	Tyr	Arg	Phe	Ser	Ala	Lys	Arg	Ala	Leu	Phe	Ile	Leu	Gly	Pro	
65		100					105				110						
67	ttt	aat	ccc	ctc	aga	agc	tta	atg	att	cgt	atc	tct	gtc	cat	tca	gtc	441
68	Phe	Asn	Pro	Leu	Arg	Ser	Leu	Met	Ile	Arg	Ile	Ser	Val	His	Ser	Val	
69	115					120				125				130			
71	ttt	agc	atg	ttc	atc	atc	tgc	acg	gtg	atc	atc	aac	tgt	atg	ttc	atg	489
72	Phe	Ser	Met	Phe	Ile	Ile	Cys	Thr	Val	Ile	Ile	Asn	Cys	Met	Phe	Met	
73					135					140				145			
75	gcg	aat	tct	atg	gag	aga	agt	ttc	gac	aac	gac	att	ccc	gaa	tac	gtc	537
76	Ala	Asn	Ser	Met	Glu	Arg	Ser	Phe	Asp	Asn	Asp	Ile	Pro	Glu	Tyr	Val	
77				150					155				160				
79	ttc	att	ggg	att	tat	att	tta	gaa	gct	gtg	att	aaa	ata	ttg	gca	aga	585
80	Phe	Ile	Gly	Ile	Tyr	Ile	Leu	Glu	Ala	Val	Ile	Lys	Ile	Leu	Ala	Arg	
81		165					170					175					
83	ggc	ttc	att	gtg	gat	gag	ttt	tcc	ttc	ctc	cga	gat	ccg	tgg	aac	tgg	633
84	Gly	Phe	Ile	Val	Asp	Glu	Phe	Ser	Phe	Leu	Arg	Asp	Pro	Trp	Asn	Trp	
85	180					185				190							
87	ctg	gac	ttc	att	gtc	att	gga	aca	gcg	atc	gca	act	tgt	ttt	ccg	ggc	681
88	Leu	Asp	Phe	Ile	Val	Ile	Gly	Thr	Ala	Ile	Ala	Thr	Cys	Phe	Pro	Gly	
89	195			200					205				210				
91	agc	caa	gtc	aat	ctt	tca	gct	ctt	cgt	acc	ttc	cga	gtg	ttc	aga	gct	729
92	Ser	Gln	Val	Asn	Leu	Ser	Ala	Leu	Arg	Thr	Phe	Arg	Val	Phe	Arg	Ala	
93				215					220				225				
95	ctg	aag	gcg	att	tca	ggt	atc	tca	ggt	ctg	aag	gtc	atc	gta	ggt	gcc	777
96	Leu	Lys	Ala	Ile	Ser	Val	Ile	Ser	Gly	Leu	Lys	Val	Ile	Val	Gly	Ala	
97			230				235					240					
99	ctg	ctg	cgc	tgc	gtg	aag	aag	ctg	gta	gac	gtg	atg	gtc	ctc	act	ctc	825
100	Leu	Leu	Arg	Ser	Val	Lys	Lys	Leu	Val	Asp	Val	Met	Val	Leu	Thr	Leu	
101		245					250				255						
103	ttc	tgc	ctc	agc	atc	ttt	gcc	ctg	gtc	ggt	cag	cag	ctg	ttc	atg	gga	873
104	Phe	Cys	Leu	Ser	Ile	Phe	Ala	Leu	Val	Gly	Gln	Leu	Phe	Met	Gly		
105	260					265				270							
107	att	ctg	aac	cag	aag	tgt	att	aag	cac	aac	tgt	ggc	ccc	aac	cct	gca	921
108	Ile	Leu	Asn	Gln	Lys	Cys	Ile	Lys	His	Asn	Cys	Gly	Pro	Asn	Pro	Ala	
109	275			280					285				290				
111	tcc	aac	aag	gat	tgc	ttt	gaa	aag	gaa	aaa	gat	agc	gaa	gac	ttc	ata	969
112	Ser	Asn	Lys	Asp	Cys	Phe	Glu	Lys	Glu	Lys	Asp	Ser	Glu	Asp	Phe	Ile	
113				295					300				305				
115	atg	tgt	ggt	acc	tgg	ctc	ggc	agc	aga	ccc	tgt	ccc	aat	ggt	tct	acg	1017
116	Met	Cys	Gly	Thr	Trp	Leu	Gly	Ser	Arg	Pro	Cys	Pro	Asn	Gly	Ser	Thr	
117			310				315					320					
119	tgc	gat	aaa	acc	aca	ttg	aac	cca	gac	aat	aat	tat	aca	aag	ttt	gac	1065
120	Cys	Asp	Lys	Thr	Thr	Leu	Asn	Pro	Asp	Asn	Asn	Tyr	Thr	Lys	Phe	Asp	
121		325					330					335					
123	aac	ttt	ggc	tgg	tcc	ttt	ctc	gcc	atg	ttc	cgg	ggt	atg	act	caa	gac	1113
124	Asn	Phe	Gly	Trp	Ser	Phe	Leu	Ala	Met	Phe	Arg	Val	Met	Thr	Gln	Asp	
125	340					345				350							
127	tcc	tgg	gag	agg	ctt	tac	cga	cag	atc	ctg	cgg	acc	tct	ggg	atc	tac	1161
128	Ser	Trp	Glu	Arg	Leu	Tyr	Arg	Gln	Ile	Leu	Arg	Thr	Ser	Gly	Ile	Tyr	

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129	355		360		365		370	
131	ttt gtc ttc ttc ttc gtg gtg gtc atc ttc ctg ggc tcc ttc tac ctg						1209	
132	Phe Val Phe Phe Phe Val Val Val Ile Phe Leu Gly Ser Phe Tyr Leu							
133		375		380		385		
135	ctt aac cta acc ctg gct gtt gtc acc atg gct tat gaa gaa cag aac						1257	
136	Leu Asn Leu Thr Leu Ala Val Val Thr Met Ala Tyr Glu Glu Gln Asn							
137		390		395		400		
139	aga aat gta gct gct gag aca gag gcc aag gag aaa atg ttt cag gaa						1305	
140	Arg Asn Val Ala Ala Glu Thr Glu Ala Lys Glu Lys Met Phe Gln Glu							
141		405		410		415		
143	gcc cag cag ctg tta agg gag gag aag gag gct ctg gtt gcc atg gga						1353	
144	Ala Gln Gln Leu Leu Arg Glu Glu Lys Glu Ala Leu Val Ala Met Gly							
145		420		425		430		
147	att gac aga agt tcc ctt aat tcc ctt caa gct tca tcc ttt tcc ccg						1401	
148	Ile Asp Arg Ser Ser Leu Asn Ser Leu Gln Ala Ser Ser Phe Ser Pro							
149	435		440		445		450	
151	aag aag agg aag ttt ttc ggt agt aag aca aga aag tcc ttc ttt atg						1449	
152	Lys Lys Arg Lys Phe Phe Gly Ser Lys Thr Arg Lys Ser Phe Phe Met							
153		455		460		465		
155	aga ggg tcc aag acg gcc caa gcc tca gcg tct gat tca gag gac gat						1497	
156	Arg Gly Ser Lys Thr Ala Gln Ala Ser Ala Ser Asp Ser Glu Asp Asp							
157		470		475		480		
159	gcc tct aaa aat cca cag ctc ctt gag cag acc aaa cga ctg tcc cag						1545	
160	Ala Ser Lys Asn Pro Gln Leu Leu Glu Gln Thr Lys Arg Leu Ser Gln							
161		485		490		495		
163	aac ttg cca gtg gat ctc ttt gat gag cac gtg gac ccc ctc cac agg						1593	
164	Asn Leu Pro Val Asp Leu Phe Asp Glu His Val Asp Pro Leu His Arg							
165		500		505		510		
167	cag aga gcg ctg agc gct gtc agt atc tta acc atc acc atg cag gaa						1641	
168	Gln Arg Ala Leu Ser Ala Val Ser Ile Leu Thr Ile Thr Met Gln Glu							
169	515		520		525		530	
171	caa gaa aaa ttc cag gag cct tgt ttc cca tgt ggg aaa aat ttg gcc						1689	
172	Gln Glu Lys Phe Gln Glu Pro Cys Phe Pro Cys Gly Lys Asn Leu Ala							
173		535		540		545		
175	tct aag tac ctg gtg tgg gac tgt agc cct cag tgg ctg tgc ata aag						1737	
176	Ser Lys Tyr Leu Val Trp Asp Cys Ser Pro Gln Trp Leu Cys Ile Lys							
177		550		555		560		
179	aag gtc ctg cgg acc atc atg acg gat ccc ttt act gag ctg gcc atc						1785	
180	Lys Val Leu Arg Thr Ile Met Thr Asp Pro Phe Thr Glu Leu Ala Ile							
181		565		570		575		
183	acc atc tgc atc atc atc aat acc gtt ttc tta gcc gtg gag cac cac						1833	
184	Thr Ile Cys Ile Ile Ile Asn Thr Val Phe Leu Ala Val Glu His His							
185		580		585		590		
187	aac atg gat gac aac tta aag acc ata ctg aaa ata gga aac tgg gtt						1881	
188	Asn Met Asp Asp Asn Leu Lys Thr Ile Leu Lys Ile Gly Asn Trp Val							
189	595		600		605		610	
191	ttc acg gga att ttc ata gcg gaa atg tgt ctc aag atc atc gcg ctc						1929	
192	Phe Thr Gly Ile Phe Ile Ala Glu Met Cys Leu Lys Ile Ile Ala Leu							
193		615		620		625		

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195	gac cct tac cac tac ttc cgg cac ggc tgg aat gtt ttt gac agc atc	1977
196	Asp Pro Tyr His Tyr Phe Arg His Gly Trp Asn Val Phe Asp Ser Ile	
197	630 635 640	
199	gtg gcc ctc ctg agt ctc gct gat gtg ctc tac aac aca ctg tct gat	2025
200	Val Ala Leu Leu Ser Leu Ala Asp Val Leu Tyr Asn Thr Leu Ser Asp	
201	645 650 655	
203	aac aat agg tct ttc ttg gct tcc ctc aga gtg ctg agg gtc ttc aag	2073
204	Asn Asn Arg Ser Phe Leu Ala Ser Leu Arg Val Leu Arg Val Phe Lys	
205	660 665 670	
207	tta gcc aaa tcc tgg ccc acg tta aac act ctc att aag atc atc ggc	2121
208	Leu Ala Lys Ser Trp Pro Thr Leu Asn Thr Leu Ile Lys Ile Ile Gly	
209	675 680 685 690	
211	cac tcc gtg ggc gcg ctt gga aac ctg act gtg gtc ctg act atc gtg	2169
212	His Ser Val Gly Ala Leu Gly Asn Leu Thr Val Val Leu Thr Ile Val	
213	695 700 705	
215	gtc ttc atc ttt tct gtg gtg ggc atg cgg ctc ttc ggc acc aag ttt	2217
216	Val Phe Ile Phe Ser Val Val Gly Met Arg Leu Phe Gly Thr Lys Phe	
217	710 715 720	
219	aac aag acc gcc tac gcc acc cag gag cgg ccc agg cgg cgc tgg cac	2265
220	Asn Lys Thr Ala Tyr Ala Thr Gln Glu Arg Pro Arg Arg Arg Trp His	
221	725 730 735	
223	atg gat aat ttc tac cac tcc ttc ctg gtg gtg ttc cgc atc ctc tgt	2313
224	Met Asp Asn Phe Tyr His Ser Phe Leu Val Val Phe Arg Ile Leu Cys	
225	740 745 750	
227	ggg gaa tgg atc gag aac atg tgg ggc tgc atg cag gat atg gac ggc	2361
228	Gly Glu Trp Ile Glu Asn Met Trp Gly Cys Met Gln Asp Met Asp Gly	
229	755 760 765 770	
231	tcc ccg ttg tgc atc att gtc ttt gtc ctg ata atg gtg atc ggg aag	2409
232	Ser Pro Leu Cys Ile Ile Val Phe Val Leu Ile Met Val Ile Gly Lys	
233	775 780 785	
235	ctt gtg gtg ctt aac ctc ttc att gcc ttg ctg ctc aat tcc ttc agc	2457
236	Leu Val Val Leu Asn Leu Phe Ile Ala Leu Leu Leu Asn Ser Phe Ser	
237	790 795 800	
239	aat gag gag aag gat ggg agc ctg gaa gga gag acc agg aaa acc aaa	2505
240	Asn Glu Glu Lys Asp Gly Ser Leu Glu Gly Glu Thr Arg Lys Thr Lys	
241	805 810 815	
243	gtg cag cta gcc ctg gat cgg ttc cgc cgg gcc ttc tcc ttc atg ctg	2553
244	Val Gln Leu Ala Leu Asp Arg Phe Arg Arg Ala Phe Ser Phe Met Leu	
245	820 825 830	
247	cac gct ctt cag agt ttt tgt tgc aag aaa tgc agg agg aaa aac tcg	2601
248	His Ala Leu Gln Ser Phe Cys Cys Lys Lys Cys Arg Arg Lys Asn Ser	
249	835 840 845 850	
251	cca aag cca aaa gag aca aca gaa agc ttt gct ggt gag aat aaa gac	2649
252	Pro Lys Pro Lys Glu Thr Thr Glu Ser Phe Ala Gly Glu Asn Lys Asp	
253	855 860 865	
255	tca atc ctc ccg gat gcg agg ccc tgg aag gag tat gat aca gac atg	2697
256	Ser Ile Leu Pro Asp Ala Arg Pro Trp Lys Glu Tyr Asp Thr Asp Met	
257	870 875 880	
259	gct ttg tac act gga cag gcc ggg gct ccg ctg gcc cca ctc gca gag	2745

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260 Ala Leu Tyr Thr Gly Gln Ala Gly Ala Pro Leu Ala Pro Leu Ala Glu
261      885      890      895
263 gta gag gac gat gtg gaa tat tgt ggt gaa ggc ggt gcc cta ccc acc      2793
264 Val Glu Asp Asp Val Glu Tyr Cys Gly Glu Gly Gly Ala Leu Pro Thr
265      900      905      910
267 tca caa cat agt gct gga gtt cag gcc ggt gac ctc cct cca gag acc      2841
268 Ser Glr His Ser Ala Gly Val Gln Ala Gly Asp Leu Pro Pro Gln Thr
269 915      920      925      930
271 aag cag ctc act agc ccg gat gac caa ggg gtt gaa atg gaa gta ttt      2889
272 Lys Gln Leu Thr Ser Pro Asp Asp Gln Gly Val Glu Met Glu Val Phe
273      935      940      945
275 tct gaa gaa gat ctg cat tta agc ata cag agt cct cga aag aag tct      2937
276 Ser Glu Glu Asp Leu His Leu Ser Ile Gln Ser Pro Arg Lys Lys Ser
277      950      955      960
279 gac gca gtg agc atg ctc tcg gaa tgc agc aca att gac ctg aat gat      2985
280 Asp Ala Val Ser Met Leu Ser Glu Cys Ser Thr Ile Asp Leu Asn Asp
281      965      970      975
283 atc ttt aga aat tta cag aaa aca gtt tcc ccc aaa aag cag cca gat      3033
284 Ile Phe Arg Asn Leu Gln Lys Thr Val Ser Pro Lys Lys Gln Pro Asp
285      980      985      990
287 aga tgc ttt ccc aag ggc ctt agt tgt cac ttt cta tgc cac aaa      3078
288 Arg Cys Phe Pro Lys Gly Leu Ser Cys His Phe Leu Cys His Lys
289 995      1000      1005
291 aca gac aag aga aag tcc ccc tgg gtc ctg tgg tgg aac att cgg      3123
292 Thr Asp Lys Arg Lys Ser Pro Trp Val Leu Trp Trp Asn Ile Arg
293 1010      1015      1020
295 aaa acc tgc tac caa atc gtg aag cac agc tgg ttt gag agt ttc      3168
296 Lys Thr Cys Tyr Gln Ile Val Lys His Ser Trp Phe Glu Ser Phe
297 1025      1030      1035
299 ata atc ttt gtt att ctg ctg agc agt gga gcg ctg ata ttt gaa      3213
300 Ile Ile Phe Val Ile Leu Leu Ser Ser Gly Ala Leu Ile Phe Glu
301 1040      1045      1050
303 gat gtc aat ctc ccc agc cgg ccc caa gtt gag aaa tta cta agg      3258
304 Asp Val Asn Leu Pro Ser Arg Pro Gln Val Glu Lys Leu Leu Arg
305 1055      1060      1065
307 tgt acc gat aat att ttc aca ttt att ttc ctc ctg gaa atg atc      3303
308 Cys Thr Asp Asn Ile Phe Thr Phe Ile Phe Leu Leu Glu Met Ile
309 1070      1075      1080
311 ctg aag tgg gtg gcc ttt gga ttc cgg agg tat ttc acc agt gcc      3348
312 Leu Lys Trp Val Ala Phe Gly Phe Arg Arg Tyr Phe Thr Ser Ala
313 1085      1090      1095
315 tgg tgc tgg ctt gat ttc ctc att gtg gtg gtg tct gtg ctc agt      3393
316 Trp Cys Trp Leu Asp Phe Leu Ile Val Val Val Ser Val Leu Ser
317 1100      1105      1110
319 ctc atg aat cta cca agc ttg aag tcc ttc cgg act ctg cgg gcc      3438
320 Leu Met Asn Leu Pro Ser Leu Lys Ser Phe Arg Thr Leu Arg Ala
321 1115      1120      1125
323 ctg aga cct ctg cgg gcg ctg tcc cag ttt gaa gga atg aag gtt      3483
324 Leu Arg Pro Leu Arg Ala Leu Ser Gln Phe Glu Gly Met Lys Val

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RAW SEQUENCE LISTING ERROR SUMMARY  
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*fyi*  
Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 5804

**VERIFICATION SUMMARY**

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:2429 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:5803